Table 3. Tumorigenic properties of CRC cells based on EpCAM and CD44 expression

Experiment no.	Tumor source*		Lin <sup>-</sup> sorted populations <sup>†</sup>	Cell dose	Tumor take <sup>‡</sup>	$P^{\S}$
1	UM#4	<i>m</i> 2	EpCAM <sup>high</sup> /CD44 <sup>+</sup> all the rest (mainly EpCAM <sup>low</sup> /CD44 <sup>-</sup> )	2,500 4,000	<b>4/5</b> 0/5	0.0218
2	UM#4	m4	EpCAM <sup>high</sup> /CD44 <sup>+</sup> all the rest (mainly EpCAM <sup>low</sup> /CD44 <sup>-</sup> )	1,000 1,000	<b>4/5</b> 0/5	n.s. (0.0624)
3	UM#4	m4	EpCAM <sup>high</sup> /CD44 <sup>+</sup> all the rest (mainly EpCAM <sup>low</sup> /CD44 <sup>-</sup> )  "	200 1,000 200 1,000	7/8 2/2 0/10 0/6	< 0.0001
4	UM#4	m4	EpCAM <sup>high</sup> /CD44 <sup>+</sup> all the rest (mainly EpCAM <sup>low</sup> /CD44 <sup>-</sup> ) "	200 1,000 200 1,000	9/10 5/5 0/10 0/8	< 0.0001
5	UM#4	m5	EpCAM <sup>high</sup> /CD44 <sup>+</sup> all the rest (mainly EpCAM <sup>low</sup> /CD44 <sup>neg</sup> )	1,000 12,000	<b>2/3</b> 0/3	0.0059
6	UM#6	m2	EpCAM <sup>high</sup> /CD44 <sup>+</sup> all the rest (mainly EpCAM <sup>low</sup> /CD44 <sup>-</sup> )	400 2,000 2,000	<b>9/10 4/4</b> 0/10	0.0001
7	UM#8	m1	CD44 <sup>+</sup> CD44 <sup>-</sup>	14,000 14,000	<b>2/5</b> 0/5	n.s. (0,2499)
8	UM#8	m1	EpCAM <sup>high</sup> /CD44 <sup>+</sup> all the rest (mainly EpCAM <sup>low</sup> /CD44 <sup>neg</sup> )	5,000 6,000	<b>4/5</b> 0/5	0,0426
9	MIC69	т6	EpCAM <sup>high</sup> /CD44 <sup>+</sup> all the rest (mainly EpCAM <sup>low</sup> /CD44 <sup>neg</sup> )	800 8,000	<b>2/5</b> 0/5	0,0082
10	OMP-C5	m1	EpCAM <sup>high</sup> /CD44 <sup>+</sup> all the rest (mainly EpCAM <sup>low</sup> /CD44 <sup>-</sup> )	400 2,000 2,000	<b>7/10 4/5</b> 0/10	0.0001
11	OMP-C8	m1	EpCAM <sup>high</sup> /CD44 <sup>+</sup> " all the rest (mainly EpCAM <sup>low</sup> /CD44 <sup>-</sup> )	200 2,000 2,000	5/10 5/5 1/10	0,0004

<sup>\*</sup>For each experiment, the *in vivo* serial passage of the tumor xenograft used as source for cancer cell purification is reported as follows: m1, first round of tumors obtained from primary tumor engraftment; m2, second round of tumors obtained from engraftment of m1; m3, third round of tumors obtained from engraftment of m2; and so on progressively; *primary*, primary tumor directly harvested from a surgical specimen.

<sup>†</sup>All sorted populations are to be considered as negative for expression of nonepithelial lineage markers (Lin¯; see *Materials and Methods*).

<sup>‡</sup>Tumor take is reported as number of tumors obtained/number of injections; tumor take is considered unsuccessful when no tumor mass is visible after 5 months follow-up.

§For each individual experiment, the *P* value indicates the probability of observing identical results as a matter of chance and is calculated using a hypergeometric distribution (see *SI Materials and Methods*). *n.s.*, not significant, indicates *P* values that do not reach statistical significance.